

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:06:44 ; Search time 17398.4 Seconds
(without alignments)
1463.857 Million cell updates/sec

Title: US-09-303-518D-463

Perfect score: 1887

Sequence: 1 ttggcattcccgcaaat.....catatccattatgatag 1887

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: em_estlba:*
2: em_estlhm:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_estlhc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_estl3:*
12: gb_estl4:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63.8	3.4	997	12	CNS005TE
2	52	2.7	1101	12	CNS0182P
3	50.2	2.7	1101	12	CNS0039G
4	49.6	2.6	1067	12	CNS00C08
5	49.2	2.6	987	12	CNS00418
6	49	2.6	938	12	CNS006TJ
7	46.4	2.5	1031	12	CNS00CF2
8	46.2	2.4	1101	12	CNS000D1
9	44.6	2.4	1034	12	CNS010B4
10	44.2	2.3	588	12	FR0037514
11	43.8	2.3	757	12	B21783
12	43.6	2.3	1031	12	CNS03NUL
13	43.4	2.3	797	12	CNS003F8
14	43.2	2.3	1101	12	CNS00F7H
15	43	2.3	1101	12	CNS0039E
16	42.8	2.3	925	12	CNS0091P
17	42.4	2.2	997	12	CNS009XQ

18	42.4	2.2	1101	12	CNS0175Y
19	42.2	2.2	467	10	BG607950
20	42.2	2.2	572	12	BH233657
21	42.2	2.2	1001	12	CNS0086G
22	41.6	2.2	693	12	AG165805
23	41.6	2.2	943	12	CNS0021M
24	41.6	2.2	1101	12	CNS0181N
25	41.4	2.2	1101	12	CNS0106X
26	41.4	2.2	1101	12	CNS017RP
27	41.2	2.2	668	9	AV895698
28	41.1	2.2	1201	12	CNS0163T
29	40.6	2.2	613	10	BG607415
30	40.6	2.2	644	10	BG607300
31	40.2	2.1	983	12	CNS014HC
32	40	2.1	918	12	CNS01L3Y
33	40	2.1	1080	12	CNS008BP
34	39.8	2.1	512	12	AO866684
35	39.8	2.1	657	10	BG810307
36	39.8	2.1	760	10	BE972622
37	39.8	2.1	1100	12	CNS008EX
38	39.6	2.1	967	12	CNS016XI
39	39.6	2.1	1101	12	CNS006G9
40	39.4	2.1	516	9	AL514527
41	39.4	2.1	651	10	BE846943
42	39.4	2.1	1204	12	CNS016B2
43	39.2	2.1	566	9	AM646687
44	39.2	2.1	681	12	CNS02EDD
45	39.2	2.1	914	12	CNS00C2P
46	39.2	2.1	872	10	BI957771
47	39	2.1	1101	12	CNS00KUZ
48	39	2.1	1201	12	CNS016DO
49	38.8	2.1	971	12	CNS016VO
50	38.8	2.1	1061	12	CNS03LHZ
51	38.8	2.1	1134	12	CNS0307D
52	38.6	2.0	690	12	AG111046
53	38.6	2.0	842	9	BE188368
54	38.6	2.0	947	12	CNS03N8T
55	38.6	2.0	997	12	CNS00K4P
56	38.6	2.0	1101	12	CNS00KRA
57	38.6	2.0	1183	12	CNS016CR
58	38.6	2.0	628	10	BI953999
59	38.4	2.0	859	12	CNS00KLT
60	38.4	2.0	864	12	CNS04NLA
61	38.4	2.0	884	10	BI956488
62	38.4	2.0	1101	12	CNS0006J
63	38.4	2.0	1101	12	CNS017KX
64	38.4	2.0	1157	9	BE036799
65	38.2	2.0	791	12	AG044973
66	38.2	2.0	797	12	AO864430
67	38.2	2.0	1033	10	BE290476
68	38.2	2.0	1101	12	CNS0039L
69	38.2	2.0	1147	12	CNS016BS
70	38.2	2.0	1201	12	CNS0107K
71	38	2.0	1101	12	CNS0007K
72	38	2.0	1101	12	CNS0100X
73	38	2.0	1101	12	CNS016HD
74	38	2.0	1101	12	CNS01768
75	37.8	2.0	463	12	AO815822
76	37.8	2.0	778	12	CNS03EXR
77	37.8	2.0	925	12	CNS002BN
78	37.8	2.0	1101	12	CNS00240
79	37.6	2.0	558	9	AM564214
80	37.6	2.0	644	10	BM164185
81	37.6	2.0	912	12	BH148448
82	37.6	2.0	1101	12	CNS010BT
83	37.6	2.0	1101	12	CNS0182T
84	37.4	2.0	456	12	AO815024
85	37.4	2.0	494	12	AO869337
86	37.4	2.0	625	9	AV924646
87	37.4	2.0	631	12	AG070440
88	37.4	2.0	668	12	AG062735
89	37.4	2.0	826	12	AO912123
90	37.2	2.0	518	10	BI568228

AL108460	Drosophila
BG607950	WHE2475_G
BH233657	1006175A0
AL062781	Drosophila
AG165805	Pan trogl
AL097720	Drosophila
AL108773	Drosophila
AL098595	Drosophila
AL108415	Drosophila
AV895698	AV895698
AL106259	Drosophila
BG607415	WHE2479_D
BG607300	WHE2493_G
AL104168	Drosophila
AL149151	Anopheles
AL069494	Drosophila
AO866684	nbe0028F
BG810307	mge0003xo
BE972622	601652519
AL069107	Drosophila
AL107328	Drosophila
AL072006	Drosophila
AL514527	AL514527
BE846943	PSB 571 L
AL106628	Drosophila
AM646687	cm67f03..w
AL193990	Tetradon
AL059740	Drosophila
BI957771	HVSMEM001
AL078268	Drosophila
AL106614	Drosophila
AL107372	Drosophila
AL249488	Tetradon
AL221890	Tetradon
AG111046	Pan trogl
BE188368	PVB 154 L
AL251739	Tetradon
AL102403	Drosophila
AL077618	Drosophila
AL106581	Drosophila
BI953999	HVSMEM001
AL077728	Drosophila
AL298855	Tetradon
BI956488	HVSMEM000
AL062049	Drosophila
AL108171	Drosophila
BE036799	MO6B03 M
AG044973	Pan trogl
AO864430	nbe0023H
BE290476	601088563
AL063926	Drosophila
AL106625	Drosophila
AL098625	Drosophila
AL062086	Drosophila
AL098379	Drosophila
AL106747	Drosophila
AL107642	Drosophila
AO815822	HS_5395.A
AL240994	Tetradon
AL074475	Drosophila
AL061823	Drosophila
AM564214	L61_285_A
BM164185	EST566708
BH148448	ENTP58TF
AL098781	Drosophila
AL108815	Drosophila
AO815024	HS_5261.A
AO869337	nbe00035E
AV924646	AV924646
AG070440	Pan trogl
AG062735	Pan trogl
AO912123	nbe00017I
BI568228	RH39634.5

91 37.2 2.0 568 10 BG608064
 92 37.2 2.0 577 9 AL504025
 93 37.2 2.0 585 12 AZ304600
 94 37.2 2.0 759 12 AG056348
 95 37.2 2.0 888 12 CENS02C98
 96 37.2 2.0 997 12 CENS0204B
 97 37.2 2.0 1002 12 CENS040AN
 98 37.2 2.0 1019 12 CENS045SN
 99 37.2 2.0 1101 12 CENS017KE
 100 37.2 2.0 1627 10 BF792678

ALIGNMENTS

RESULT 1
 LOCUS CENS05TE/c 997 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL060767.1 GI:4943573
 VERSION AL060767
 KEYWORDS fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 997)
 AUTHORS Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Oosawa and
 Aaron Mammosier in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
 source Location/Qualifiers
 1. 997
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR12K22"
 /note="end : TET3"
 BASE COUNT 89 a 99 c 13 g 258 t 538 others
 ORIGIN

Query Match 3.4%; Score 63.8; DB 12; Length 997;
 Best Local Similarity 19.5%; Pred. No. 1.8e-05;
 Matches 98; Conservative 174; Mismatches 231; Indels 0; Gaps 0;

QY 1369 agatggggggtgttaggaagcctaataatgcaactcgtgagcggtggagagaat 1428
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 997 AKRARRRGAARARARARRRRRRGARRGARRRARRRRARRRARRRARRRAG 938
 QY 1429 gtcaagaaacgaagaaagagtcagagtcagtttaagccatgcgaacgagaa 1488
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 937 AGAARAAARRRRARRRRRRRAGRRAGRRAGRRGRRGRRRAAARARARARARAR 878

QY 1489 tgggaataaacaaggttagatttaacattatagtggtgtatatacaataagaa 1548
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 877 ARRRARRKARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRAGA 818
 QY 1549 ggaacagtaacagagagcagtaaccccggtgagtcaggtgatacagcaaac 1608
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 817 ARARARRRRARRRARA 758
 QY 1609 tcggacactataacatggtgtttatcaagcgacgtggaatataaagcctatga 1668
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 757 RARARARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRAGA 698
 QY 1669 agttggaggttgaaacgaaggttggaagtgatgacacgacacccattccca 1728
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 697 ARRRRRRRGAGARRRA 638
 QY 1729 aagatgtgagtgagcctagtaattaggtcgaactcgtggttggaagtagaata 1788
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 637 RGARRAGA 578
 QY 1789 atgcttaagatataatgagcaggtgacagtaaatcggtatttaataagagatt 1848
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 577 RRGRRAR 518
 QY 1849 accgaacctaatagaacagcata 1871
 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 517 RRR 495

RESULT 2
 LOCUS CENS0182P 1101 bp DNA linear GSS 26-JUL-1999
 DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
 BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL108811.1 GI:5629115
 VERSION AL108811
 KEYWORDS fruit fly.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
 AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelBAC11.

FEATURES
 source Location/Qualifiers
 1. 1101
 /organism="Drosophila melanogaster"
 /plasmid="pBelBAC11"
 /db_xref="taxon:7227"
 /clone_lib="DrosBAC"
 /clone="BACN37D10"
 /note="end : SP6"
 BASE COUNT 274 a 268 c 128 g 73 t 358 others
 ORIGIN

Query Match 2.8%; Score 52; DB 12; Length 1101;
 Best Local Similarity 18.5%; Pred. No. 0.022;
 Matches 66; Conservative 152; Mismatches 136; Indels 0; Gaps 0;

COMMENT

```

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="Rpci-98"
/clone="BACR08K10"
/note="end : TET3"
201 a      64 c      131 g      202 t      503 others

```

Query Match	2.78;	Score 50.2;	DB 12;	Length 1101;
Best Local Similarity	14.48;	Pred. No. 0.063;		

[illegible]

COMMENT

The BDPG is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDPG *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osoegawa and

LOCUS	CNS06TJ	938 bp	DNA	linear	GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR4J11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL065906				
VERSION	AL065906.1	GI:4944874			
KEYWORDS	GSS.				
SOURCE	fruit fly.				
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 938)				
AUTHORS	Direct Submission				
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequence				
JOURNAL	Bp 191 91006 EVRY cedex - FRANCE (E-mail : segreifgenoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.				
FEATURES	source				
	1..938				
	/organism="Drosophila melanogaster"				
	/db_xref="taxon:7227"				
	/clone_lib="RPCI-98"				
	/clone="BACR4J11"				
	/note="end : 17"				
BASE COUNT	86 a 98 c 85 g 334 t 335 others				
ORIGIN					
Query Match	2.6%; Score 49; DB 12; Length 938;				
Best Local Similarity	21.9%; Pred. No. 0.12;				
Matches	105; Conservative 145; Mismatches 230; Indels 0; Gaps 0;				
Oy	1387 aagctaatattgacaactcgtgaacgcggcgaggagaatagttcagaagaacgagaaga	1446			
	::: ::: ::: ::: ::: ::: ::: :::				
Dd	936 AAKAADTAAGAADAADKADKADGAGAAADAAMAARADKKDRADKADRAADDDKDXR	877			
Oy	1447 aggaagtcagagtagtcagtgttaagcccaatgycgacagcagaaatggygaataaacaag	1506			
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Dd	876 KAKAKKKKKAKKKKKADKDKAKKKAKKKAKKADKMWRKAKKADADAADAKAKAKAAAAMW	817			
Oy	1507 tttagtlttaatcatlitttagtggtgatcatacaataagaagcgcagtaacgagaagg	1566			
	: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Dd	816 KMKWKDADADDAAADKADKADKADKADKADDAADADADKDKKKKDADAADAKADDA	757			
Oy	1567 catagcttaaccgggtgatgatgacgggagatcacaaaacacctcgccacctgtaaacat	1626			
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Dd	756 DAATAAKADRRADKADAGDKAKAANAADDDKARFADAKAKAAADKDKDAADRDADKA	697			
Oy	1627 ggaggttatcaagcgacagctggaataaagaagcctgatggaagtggaggtgaacag	1686			
	gggg ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Dd	696 KDKMWAADDKDRAAKRRAAAAAMAWMAAADDDKARFADAKAKAAADKDKDAADKDK	637			
Oy	1687 aaaaaagcggggaagatgtagccaagcacacatgttcccagaagatgggagtgaggt	1746			
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Dd	636 AAARAQAKDKDKDAGCTATTKAAAAAAKAKKAKAKADDTTTTKTWDAATATDKKTGDGT	577			
Oy	1747 agaattagggctgaagtlacttcggtctggggaagatagaataatgcttaagataataa	1806			

[illegible]

QY 1467 taagcccatgctgcgaacgagaatgggaaataaacaagggttagatttaacatttat 1526
 Db 457 TAAATTAATACGAAACGGGAAAGAAAACCAACCGTATATTGTGAATTGCTTAA 398
 QY 1527 aggtgtgatacatcaataagaa 1548
 Db 397 AGGTGAAGATATTGATTCAAA 376
 RESULT 12
 CNS03NUL
 LOCUS 1031 bp DNA linear GSS 17-MAY-2000
 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 04D08 of library G from Tetraodon nigroviridis, genomic survey sequence.
 ACCESSION AL252534 GI:7973546
 VERSION 1
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
 REFERENCE 1 (bases 1 to 1031)
 AUTHORS Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizesmes,C., Fisher,C., Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1031)
 AUTHORS Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesmes,C., Winkler,P., Brotlier,P., Queller,F., Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1031)
 AUTHORS Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
 FEATURES
 source
 1. 1031
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="04D08"
 /clone_1lb="G"
 /note="Genoscope sequence ID : COBG040DB04LP1-end : T7"
 BASE COUNT 425 a 134 c 285 g 142 t 45 others
 ORIGIN
 Query Match 2.3%; Score 43.6; DB 12; Length 1031;
 Best Local Similarity 40.0%; Pred. No. 3.1;
 Matches 172; Conservative 17; Mismatches 241; Indels 0; Gaps 0;
 QY 1415 aggtgtgaaataatgttcaagaacgagaagagtcagatagtcagtttaagccc 1474
 Db 514 AGAGAGAGAGAGAGARAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGARR 573
 QY 1475 atgcaacgagaatgggaaataaacaaggttagatttaacatttatagtgty 1554
 Db 574 RRGGAAGAGAAAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 633
 QY 1535 atatacaagaagcagtaacagagagcagatagtcacccgtgtatgtacggg 1594
 Db 634 AAAAAAAAAAR 693

QY 1595 tgatcacacaacacctgcgcacctgataaacaatgggtttatcaagcagatggaaatla 1654
 Db 694 GAG 753
 QY 1655 aaaaagctgtatggaatgttggaagtgaaacgaaggtgggaagtgatgaccagc 1714
 Db 754 RAAAGAAAGGAGGAG 813
 QY 1715 acaccatgtcccaaaagattggatgagctagaattaggtcagttacttgctt 1774
 Db 814 AAGGAG 873
 QY 1775 gggaaatgagataatgttcaagataaataatgcaaggtgataatcgggtatla 1834
 Db 874 GRAAAAGRAAAAGAGRAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 933
 QY 1835 aaatagaag 1844
 Db 934 GAAAGAGAGG 943
 RESULT 13
 CNS003F8
 LOCUS 797 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08C03 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL064634 GI:4941986
 VERSION 1
 KEYWORDS GSS: fruit fly.
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 797)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
 source
 1. 797
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_1lb="RPCI-98"
 /clone="BACR08C03"
 /note="end : TET3"
 BASE COUNT 170 a 78 c 89 g 133 t 327 others
 ORIGIN
 Query Match 2.3%; Score 43.4; DB 12; Length 797;
 Best Local Similarity 14.8%; Pred. No. 3.1;
 Matches 48; Conservative 143; Mismatches 133; Indels 0; Gaps 0;
 QY 1557 aacagagagcagtcacccgtgtgtatgtacgggtgatacaaacacctgcgacc 1616
 Db 1557 aacagagagcagtcacccgtgtgtatgtacgggtgatacaaacacctgcgacc 1616

	Matches	118:	Conservative	0:	Mismatches	128:	Indels	0:	Gaps	0:
OY	1536	gatacaacaacacttcggccactcgatataacatcagtggtttatcaagcagacagtggaatttaa	1655							
Db	90	GAATAATAGTATACATCAAAACCGTGTAAATTCATATTTAAATTCGACACGATGTTACCA	149							
OY	1656	aagcctcgatggaagcttggaggtgaaacgcgaaaaaagtgggagaaagtatgataccaagca	1715							
Db	150	ATAATTTGAAATTAATTTATAGTGTTCGACGAAATATATTGGAAAAATTAATAACATATT	209							
OY	1716	caccatgttcccaaaaagatggatggaatgagcgctagaattaaagctgaagttaacttcggcttg	1775							
Db	210	AGCTAGGTCACCTTGGTATTTATTAATATAGCTAAGAACTTAAGACCAAAAACACACCCAGGAAA	269							
OY	1776	ggaagaatgaataatcgcttaagaatcaataataatggcagggatcaagaatcgggtattaa	1835							
Db	270	ATAATAGTCACACCATATATATATAATCAAAAATAATTGCAGAAAACAAAACCTCTTTTAAATG	329							
OY	1836	aataga	1841							
Db	330	AATAAA	335							

RESULT	28
CNS0163T	
LOCUS	1201 bp DNA
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BAON18K09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL106259
VERSION	ALI06259.1 GI:5620976
KEYWORDS	GSS.
SOURCE	Fruit fly.

ORGANISM Drosophila melanogaster
Eukaryota Metazoa: Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (23-JUL-1999) genome - Centre National de Sequençage :

COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de séquençage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk/>. This *Drosophila melanogaster* BAC
library (Dros BAC) was made by Alain Billard at CPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBlot19.1.

FEATURES	Location/Qualifiers
source	1. .1201

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/organism="Drosophila melanogaster"
/plasmid="pBelBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15K09"
/note="end : T7"

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BASE COUNT	454 a	123 c	198 g	264 t	162 others
ORIGIN					

Query Match	2.2%	Score 41	DB 12	Length 1201
Best Local Similarity	32.6%	Pred. No. 16		
Matches 114	Conservative 57	Mismatches 179	Indels 0	Gaps 0

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QY 1493 aaataaaacaggttagatttaacatttatagtggtgatacaataagaagca 155
      ||:| : | :|| | ||::: ::: | :|| ||: |
Db 805 WAAATTTTWWAWMAAATTAATAATTTTWWWWWTGKDDAAATTTWWAAAAAAGA 864
```

QY 1553 caagtaacagcagcgcatagttctaaccgctggtgatgtacgcggtatatacaacaacctcg 1612
|::||| || | : || | || | | : | | | | :
|::||| || | : || | || | | : | | | | :

Db	865	AAATAAAGGAAAAAATAAATAAATAAAGGAAATTCATTCGRRGACGAAGAAAGGHWK	924
Oy	1613	caactgataaacatgggtgtttacaaagcgacagtgtgaaatlaaaagcctgatggaagt	1672
Db	925	GRGRGTAAGAAAGCGGAAAAAGRAAARGGCGGRRGGGGAADARRKAATGGGAAAA	984
Oy	1673	ggagagtgaaacagaaanaagctggtgaaagtatgacgaagcacaccatggtcccaag	1732
Db	965	RAAATAAAATADAAAAAAGCGRRRAAAAAAAGRAGGNAAAAAATAAAAAAATAAAR	1044
Oy	1733	atctgagatgagctagaataagctgaaagttaactctggcttgggaaagtagaataatgc	1792
Db	1045	RRRGGRAAARRRRRRGGCGRRGARAANTWYRRGCGGAAAGRRRAAAGGCGAAAGC	1104
Oy	1793	ttaaagataataatggcagagtgacagaatlaalcggttataaataaa	1842
Db	1105	GGAATATATAAAAAAARARRRRRAAAAAAATAAAAAAARAAATRA	1154

RESULT	29				
LOCUS	BG607415	613 bp	mRNA	linear	EST 17-APR-2001
DEFINITION	BG607415 WHE2479.D10.G19Z5 Trifolium monococtum early reproductive apex cDNA library Trifolium monococtum cDNA WHE2479.D10.G19, mRNA sequence.				
ACCESSION	BG607415				
VERSION	BG607415.1	GI:13657398			
KEYWORDS	EST.				
SOURCE	Trifolium monococtum.				

ORGANISM
Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticaceae; Triticum.

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 613)		
Anderson, O. D.,	Chao, S.,	Dubcovsky, J.,
Echenique, V.,	Han, P. S.,	Hsia
C. C.,	Kang, Y.,	Lazo, G. R.,
Miller, R.,	Rausch, C. J.,	Seaton, C. L.,
Stamova, B.,	and Tong, J. C.	
The structure and function of the expressed portion of the wheat		

JOURNAL Unpublished (2001)
COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: candersen@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES	Location/Qualifiers
source	1. .613

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/organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHE2479_D10_G19"
/clone_lib="Triticum monococcum early reproductive apex
cdna library"
/tissue_type="Early reproductive apex"
/dev_stage="Seven week-old plants"

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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and
poly(A) RNA were prepared from apex at double-ridge stage
to terminal-spikelet stage during transition from
```

BASE COUNT	other authors).	"
133 a	232 c	148 g 100 t

/clone.lib="RPCI-98"
/clone="BACR29N07"
/note="end : TEST"
BASE COUNT 171 a 105 c 219 g 225 t 360 others
ORIGIN

Query Match 2.1%; Score 40; DB 12; Length 1080;
Best Local Similarity 19.4%; Pred. No. 27;
Matches 90; Conservative 162; Mismatches 211; Indels 0; Gaps 0;

OY 1233 gaagaagcgcgaacgttgcaggaaggttcgcgaatttggaagcagcgaataa 1292
Db 574 KAWDRKTMTWTWTKGTTGAGRWMAAGADWTTTRTIDGAAATGTTKMWAGRGKMDKKKT 633
OY 1293 tgaagaagccgcgaattcgaagaatttcggggggcggttaactaagcgaacccgt 1352
Db 634 KKTAKGTMTWTKGTTGAGRWMAAGADWTTTRTIDGAAATGTTKMWAGRGKMDKKKT 633
OY 1353 gtttgatcgaaacgcgaatgaggttagaagacttaataatgacaactcgta 1412
Db 694 KRRDRAGGKGGGTGTTDKGDDWMAADATDWTKKKDDTTWGGDATTDRMMWGMWMAADD 753
OY 1413 gcaagtgagaaataatgtcaggaagcgaagagagtcagagtcagtttaagc 1472
Db 754 DDMWAGRGAAAGADRDADARMAARAKDKTTAMATDWTTRKTRTDPTDGTGGRKR 813
OY 1473 ccattgcgaagagatggaataataaagcaggttagatttaatttaattagtg 1532
Db 814 GKGWGRKRGAGGAGTRKRGAGKGTIDAAAAMAGDTRTADTCTTTTATTTATTTK 873
OY 1533 tgatatcaataaagaagcagatagcagagagcagtcgaacccgtgtgtagt 1592
Db 874 GAGTDDTKMKATADATATAKRMRKDRAPRTAMAKAGDMKADGKRKRTAGDRG 933
OY 1593 ggtgtacacaaacctgcgcacccgataaactgggtttatcaagcagcagtg 1652
Db 934 AAATRTWCAADTTTWTGKMGWRAGAGGWRMDKMDKGTAKTGDGTCTGTTGCGT 993
OY 1653 taagaacctgataagtgagtggaagtgaaacgaagaaagtg 1695
Db 994 ATAGRAGWKGRRKRGKDRKTRRRARRGRGDKAKMDTGGGT 1036

RESULT 34
LOCUS A0866684 512 bp DNA linear GSS 03-NOV-1999
DEFINITION nbe0028F16f CUGI Rice BAC Library (ECORI) Oryza sativa genomic
clone nbe0028F16f, DNA sequence.
ACCESSION A0866684
VERSION A0866684.1 GI:6217141
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 512)
AUTHORS Wang, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wang RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rtwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 28
High quality sequence stop: 177.
Location/Qualifiers

FEATURES

source

1. 512
/organism="Oryza sativa"
/strain="Japanica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbe0028F16f"
/clone.lib="CUGI Rice BAC Library (ECORI)"
/tissue="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBACindigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9%. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
BASE COUNT 107 a 157 c 175 g 68 t 5 others
ORIGIN

Query Match 2.1%; Score 39.8; DB 12; Length 512;
Best Local Similarity 48.9%; Pred. No. 21;
Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

OY 574 gccgcgcctatgctgaagcagaagtagtgcgcaggttaacagcgcacccgatac 633
Db 425 GCCGCCGCCGCCGCCGCCGGAAGAACGCGCAGCGAGCGGCCGCCGCCGCCGCCGCC 366
OY 634 ccgagctggagcagatgcgcgcgaatgcgcgaagccttcgaagcagtcagatcgc 693
Db 365 ACCGCGCCCTCGACGCTCGCCGCCGCCGCCGCCACCTCTCCGCTGGGGAATTCAC 306
OY 694 aaaaacatcgcgcgcgcgcgaagaattgtcgcgcagcagtcgctgcagggatata 753
Db 305 GCGGCCGCTCTCCGCTCGAGGGAAGAACTCACGCGCGCGCGCGGAGCGGAACGGAG 246
OY 754 agcgaagcgtcaaatgtgtcgcacagcaggttggt 792
Db 245 GCGGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCCATCAGT 207

RESULT 35
LOCUS BG810307 657 bp mRNA linear EST 22-MAY-2001
DEFINITION mgct003x006f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
grisea cDNA clone mgct003x006f 5', mRNA sequence.
ACCESSION BG810307
VERSION BG810307.1 GI:14181287
KEYWORDS EST.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 657)
AUTHORS Choi, W. and Dean, R.A.
TITLE Construction and sequence analysis of an appressorium stage cDNA
JOURNAL library in the rice blast fungus, Magnaporthe grisea
COMMENT Unpublished (2001)
Contact: Ralph A. Dean

Db	992	AMKMKDKKKAKKAAKMKKKDKKKDKKKKKKKKKKKKKKKKKAAKDAAAAAAANKK	933
Oy	1614	acctgtaaacatggggttatcaagcg--accagtgaataataaaaagccctatgtaagt	1671
Db	932	DKKKDAAKAAKAKKKKKDDAAKRRKAKKKDDAADADAAKAAKRAKKDKKKDADDKRA	873
Oy	1672	tggtagtgtaaacaagaaaaaggltggaagaatgatgccaacacacactgttcccnaa	1731
Db	872	AADAARAKKKDKAAKADKAAKDAAKWKDKKAGGARAARAAKCKGGCRKGAGCGAAAA	813
Oy	1732	gatttgatgatgccta--gaattaggtcgaagttaacttcggttcgttggaaatgaata	1789
Db	812	GATTTWATKTDTTKKAGDAKTTTTTCKTTTWATKGAAGAKKTRAAKARDGARDAATPAK	753
Oy	1790	tgcttaagatatataatgycaggtgacagtaaatcsgtgtttaaatagaagattta	1849
Db	752	AARAAGAATAATKCGGAARRAGGAAGKDGARAKAAKAAKAGATRKGAATAATCAKMAAGRAW	693
Oy	1850	ccgaacctaatagaaca	1866
Db	692	ACMATATGWATRGAAGA	676
RESULT	43		
LOCUS	AM646687/c	566 bp mRNA linear EST 26-APR-2001	
DEFINITION	cm6f03.w1 Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX016F03 5', mRNA sequence.		
ACCESSION	AM646687		
VERSION	AM646687.1	GI:7404183	
KEYWORDS	EST.		
SOURCE	African clawed frog.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.		
AUTHORS	1 (bases 1 to 566) Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G. Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman J.W., Bonaldo,M.F. and Soares,M.B. The NIHES Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs		
TITLE	Gene 267 (1), 71-87 (2001)		
JOURNAL	21211403		
MEDLINE	Contact: Perry J. Blackshear		
COMMENT	Office of Clinical Research and Laboratory of Signal Transduction National Institute of Environmental Health Sciences A2-05 NIHES, 101 Alexander Drive, Research Triangle Park, NC 27709, USA Tel.: 919 541-4899 Fax: 919 541-4571 Email: black009@niehs.nih.gov Clone is available through Research Genetics, Inc., 2130 Memorial Parkway, Huntsville, AL 35901 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email cdna@resgen.com DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC). PCR Primers FORWARD: TGTAAACGACGGCCACT BACKWARD: CAGGAACAGCTATGCC Plate: 0166 row: F column: 03 Seq primer: T7 primer. Location/Qualifiers 1..566 /organism="Xenopus laevis" /db_xref="taxon:8135" /clone="PBX016F03" /clone_id="Blackshear/Soares normalized Xenopus egg library" /sex="female" /tissue_type="unfertilized egg" /cell_type="unfertilized egg"		
FEATURES			
source			

